

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lau, Lester F.
- (ii) TITLE OF INVENTION: Extracellular Matrix Signalling Molecules
- (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 - (B) STREET: 6300 Sears Tower, 233 South Wacker Drive
 - (C) CITY: Chicago
 - (D) STATE: Illinois
 - (E) COUNTRY: United States of America
 - (F) ZIP: 60606-6402
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Clough, David W.
 - (B) REGISTRATION NUMBER: 36,107
 - (C) REFERENCE/DOCKET NUMBER: 28758/33766
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 312/474-6300,
 - (B) TELEFAX: 312/474-0448
 - (C) TELEX: 25-3856

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 180..1316
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (D) OTHER INFORMATION: "Mouse cyr61 cDNA coding sequence"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGAGAGCGCC CCAGAGAAC GCCTGCAATC TCTGCGCCTC CTCCGCCAGC ACCTCGAGAG

60

AAGGACACCC GCCGCCTCGG CCCTCGCCTC ACCGCACTGC GGGCGCATTT GATCCCGCTG

120

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CTCGCCGGCT	TGTTGGTTCT	GTGTCGCCGC	GCTCGCCCCG	GTTCCCTCCTG	CGCGCCACAA	179
ATG AGC TCC AGC ACC TTC AGG ACG CTC GCT GTC	GCC GTC ACC CTT CTC					227
Met Ser Ser Ser Thr Phe Arg Thr Leu Ala Val	Ala Val Thr Leu Leu					
1	5	10			15	
CAC TTG ACC AGA CTG GCG CTC TCC ACC TGC CCC	GCC GGC TGC CAC TGC					275
His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro	Ala Ala Cys His Cys					
20	25		30			
CCT CTG GAG GCA CCC AAG TGC GCC CCG GGA GTC	GGG TTG GTC CGG GAC					323
Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val	Gly Leu Val Arg Asp					
35	40		45			
GGC TGC GGC TGC TGT AAG GTC TGC GCT AAA CAA	CTC AAC GAG GAC TGC					371
Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln	Leu Asn Glu Asp Cys					
50	55		60			
AGC AAA ACT CAG CCC TGC GAC CAC ACC AAG GGG	TTG GAA TGC AAT TTC					419
Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly	Leu Glu Cys Asn Phe					
65	70		75		80	
GGC GCC AGC TCC ACC GCT CTG AAA GGG ATC TGC	AGA GCT CAG TCA GAA					467
Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys	Arg Ala Gln Ser Glu					
85	90		95			
GGC AGA CCC TGT GAA TAT AAC TCC AGA ATC TAC	CAA AAC GGG GAA AGC					515
Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr	Gln Asn Gly Glu Ser					
100	105		110			
TTC CAG CCC AAC TGT AAA CAC CAG TGC ACA TGT	ATT GAT GGC GCC GTG					563
Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys	Ile Asp Gly Ala Val					
115	120		125			
GGC TGC ATT CCT CTG TGT CCC CAA GAA CTG TCT	CTC CCC AAT CTG GGC					611
Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser	Leu Pro Asn Leu Gly					
130	135		140			
TGT CCC AAC CCC CGG CTG GTG AAA GTC AGC	GGG CAG TGC TGT GAA GAG					659
Cys Pro Asn Pro Arg Leu Val Lys Val Ser Gly	Gln Cys Cys Glu Glu					
145	150		155		160	
TGG GTT TGT GAT GAA GAC AGC ATT AAG GAC	TGC CTG GAC GAC CAG GAT					707
Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Ser	Leu Asp Asp Gln Asp					
165	170		175			
GAC CTC CTC GGA CTC GAT GCC TCG GAG GTG	GAG TTA ACG AGA AAC AAT					755
Asp Leu Leu Gly Leu Asp Ala Ser Glu Val Glu	Leu Thr Arg Asn Asn					
180	185		190			
GAG TTA ATC GCA ATT GGA AAA GGC AGC TCA CTG	AAG AGG CTT CCT GTC					803
Glu Leu Ile Ala Ile Gly Lys Gly Ser Ser Leu	Lys Arg Leu Pro Val					
195	200		205			
TTT GGC ACC GAA CCG CGA GTT CTT TTC AAC CCT	CTG CAC GCC CAT GGC					851
Phe Gly Thr Glu Pro Arg Val Leu Phe Asn Pro	Leu His Ala His Gly					
210	215		220			
CAG AAA TGC ATC GTT CAG ACC ACG TCT TGG	TCC CAG TGC TCC AAG AGC					899
Gln Lys Cys Ile Val Gln Thr Ser Trp Ser Gln	Cys Ser Lys Ser					
225	230		235		240	
TGC GGA ACT GGC ATC TCC ACA CGA GTT ACC AAT	GAC AAC CCA GAG TGC					947

Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn. Asp Asn Pro Glu Cys			
245	250	255	
CGC CTG GTG AAA GAG ACC CGG ATC TGT GAA GTG CGT CCT TGT GGA CAA			
Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln			
260	265	270	
CCA GTG TAC AGC AGC CTA AAA AAG GGC AAG AAA TGC AGC AAG ACC AAG			
Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys			
275	280	285	
AAA TCC CCA GAA CCA GTC AGA TTT ACT TAT GCA GGA TGC TCC AGT GTC			
Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val			
290	295	300	
AAG AAA TAC CGG CCC AAA TAC TGC GGC TCC TGC GTA GAT GGC CGG TGC			
Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys			
305	310	315	320
TGC ACA CCT CTG CAG ACC AGA ACT GTG AAG ATG CGG TTC CGA TGC GAA			
Cys Thr Pro Leu Gln Thr Arg Thr Val Lys Met Arg Phe Arg Cys Glu			
325	330	335	
GAT GGA GAG ATG TTT TCC AAG AAT GTC ATG ATG ATC CAG TCC TGC AAA			
Asp Gly Glu Met Phe Ser Lys Asn Val Met Met Ile Gln Ser Cys Lys			
340	345	350	
TGT AAC TAC AAC TGC CCG CAT CCC AAC GAG GCA TCG TTC CGA CTG TAC			
Cys Asn Tyr Asn Cys Pro His Pro Asn Glu Ala Ser Phe Arg Leu Tyr			
355	360	365	
AGC CTA TTC AAT GAC ATC CAC AAG TTC AGG GAC TAAAGTGCCTC CAGGGTTCCCT			
Ser Leu Phe Asn Asp Ile His Lys Phe Arg Asp			
370	375		
AGTGTGGGCT GGACAGAGGA GAAGCGCAAG CATCATGGAG ACGTGGGTGG GCGGAGGATG			
AATGGTGCCT TGCTCATTCT TGAGTAGCAT TAGGGTATTT CAAAACTGCC AAGGGGCTGA			
TGTGGACGGA CAGCAGCGCA GCCG			
		1480	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: "Mouse Cyr61 amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Ser Ser Thr Phe Arg Thr Leu Ala Val Ala Val Thr Leu Leu			
1	5	10	15

His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys		
20	25	30

Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp.

35	40	45	
Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys			
50	55	60	
Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe			
65	70	75	80
Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu			
85	90	95	
Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser			
100	105	110	
Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val			
115	120	125	
Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly			
130	135	140	
Cys Pro Asn Pro Arg Leu Val Lys Val Ser Gly Gln Cys Cys Glu Glu			
145	150	155	160
Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Ser Leu Asp Asp Gln Asp			
165	170	175	
Asp Leu Leu Gly Leu Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn			
180	185	190	
Glu Leu Ile Ala Ile Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val			
195	200	205	
Phe Gly Thr Glu Pro Arg Val Leu Phe Asn Pro Leu His Ala His Gly			
210	215	220	
Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser			
225	230	235	240
Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys			
245	250	255	
Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln			
260	265	270	
Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys			
275	280	285	
Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val			
290	295	300	
Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys			
305	310	315	320
Cys Thr Pro Leu Gln Thr Arg Thr Val Lys Met Arg Phe Arg Cys Glu			
325	330	335	
Asp Gly Glu Met Phe Ser Lys Asn Val Met Met Ile Gln Ser Cys Lys			
340	345	350	
Cys Asn Tyr Asn Cys Pro His Pro Asn Glu Ala Ser Phe Arg Leu Tyr			
355	360	365	
Ser Leu Phe Asn Asp Ile His Lys Phe Arg Asp			

370

375

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 124..1266

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: "Human cyr61 cDNA coding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGCAGGGCCC ACCGCGACAC CGCGCCGCCA CCCCCACCCC GCTGCGCACG GCCTGTCCGC	60
TGCACACCAG CTTGTTGGCG TCTTCGTCGC CGCGCTCGCC CCGGGCTACT CCTGCGCGCC	120
ACA ATG AGC TCC CGC ATC GCC AGG GCG CTC GCC TTA GTC GTC ACC CTT Met Ser Ser Arg Ile Ala Arg Ala Leu Ala Leu Val Val Thr Leu	168
1 5 10 15	
CTC CAC TTG ACC AGG CTG GCG CTC TCC ACC TGC CCC GCT GCC TGC CAC Leu His Leu Thr Arg Leu Ala Ser Thr Cys Pro Ala Ala Cys His	216
20 25 30	
TGC CCC CTG GAG GCG CCC AAG TGC GCG CCG GGA GTC GGG CTG GTC CGG Cys Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg	264
35 40 45	
GAC GGC TGC GGC TGC TGT AAG GTC TGC GCC AAG CAG CTC AAC GAG GAC Asp Gly Cys Gly Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp	312
50 55 60	
TGC AGC AAA ACG CAG CCC TGC GAC CAC ACC AAG GGG CTG GAA TGC AAC Cys Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn	360
65 70 75	
TTC GGC GCC AGC TCC ACC GCT CTG AAG GGG ATC TGC AGA GCT CAG TCA Phe Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser	408
80 85 90 95	
GAG GGC AGA CCC TGT GAA TAT AAC TCC AGA ATC TAC CAA AAC GGG GAA Glu Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu	456
100 105 110	
AGT TTC CAG CCC AAC TGT CAA CAT CAG TGC ACA TGT ATT GAT GGC GCC Ser Phe Gln Pro Asn Cys Gln His Gln Cys Thr Cys Ile Asp Gly Ala	504
115 120 125	
GTG GGC TGC ATT CCT CTG TGT CCC CAA GAA CTA TCT CTC CCC AAC TTG Val Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu	552
130 135 140	
GGC TGT CCC AAC CCT CGG CTG GTC AAA GTT ACC GGG CAG TGC TGC GAG	600

Gly Cys Pro Asn Pro Arg Leu Val Lys Val Thr Gly Gln Cys Cys Glu	
145 150 155	
GAG TGG GTC TGT GAC GAG GAT AGT ATC AAG GAC CCC ATG GAG GAC CAG	648
Glu Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Pro Met Glu Asp Gln	
160 165 170 175	
GAC GGC CTC CTT GGC AAG GAG CTG GGA TTC GAT GCC TCC GAG GTG GAG	696
Asp Gly Leu Leu Gly Lys Glu Leu Gly Phe Asp Ala Ser Glu Val Glu	
180 185 190	
TTG ACG AGA AAC AAT GAA TTG ATT GCA GTT GGA AAA GGC AGA TCA CTG	744
Leu Thr Arg Asn Asn Glu Leu Ile Ala Val Gly Lys Gly Arg Ser Leu	
195 200 205	
AAG CGG CTC CCT GTT TTT GGA ATG GAG CCT CGC ATC CTA TAC AAC CCT	792
Lys Arg Leu Pro Val Phe Gly Met Glu Pro Arg Ile Leu Tyr Asn Pro	
210 215 220	
TTA CAA GGC CAG AAA TGT ATT GTT CAA ACA ACT TCA TGG TCC CAG TGC	840
Leu Gln Gly Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys	
225 230 235	
TCA AAG ACC TGT GGA ACT GGT ATC TCC ACA CGA GTT ACC AAT GAC AAC	888
Ser Lys Thr Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn	
240 245 250 255	
CCT GAG TGC CGC CTT GTG AAA GAA ACC CGG ATT TGT GAG GTG CGG CCT	936
Pro Glu Cys Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro	
260 265 270	
TGT GGA CAG CCA GTG TAC AGC AGC CTG AAA AAG GGC AAG AAA TGC AGC	984
Cys Gly Gln Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser	
275 280 285	
AAG ACC AAG AAA TCC CCC GAA CCA GTC AGG TTT ACT TAC GCT GGA TGT	1032
Lys Thr Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys	
290 295 300	
TTG AGT GTG AAG AAA TAC CGG CCC AAG TAC TGC GGT TCC TGC GTG GAC	1080
Leu Ser Val Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp	
305 310 315	
GGC CGA TGC TGC ACG CCC CAG CTG ACC AGG ACT GTG AAG ATG CGG TTC	1128
Gly Arg Cys Cys Thr Pro Gln Leu Thr Arg Thr Val Lys Met Arg Phe	
320 325 330 335	
CGC TGC GAA GAT GGG GAG ACA TTT TCC AAG AAC GTC ATG ATG ATC CAG	1176
Arg Cys Glu Asp Gly Glu Thr Phe Ser Lys Asn Val Met Met Ile Gln	
340 345 350	
TCC TGC AAA TGC AAC TAC AAC TGC CCG CAT GCC AAT GAA GCA GCG TTT	1224
Ser Cys Lys Cys Asn Tyr Asn Cys Pro His Ala Asn Glu Ala Ala Phe	
355 360 365	
CCC TTC TAC AGG CTG TTC AAT GAC ATT CAC AAA TTT AGG GAC	1266
Pro Phe Tyr Arg Leu Phe Asn Asp Ile His Lys Phe Arg Asp	
370 375 380	
TAAATGCTAC CTGGGTTTCC AGGGCACACC TAGACAAACA AGGGAGAAGA GTGTCAGAAT	1326
CAGAATCATG GAGAAAATGG GCGGGGGTGG TGTGGGTGAT GGGACTCATT GTAGAAAGGA	13.86

AGCCTTCTCA TTCTTGAGGA GCATTAAGGT AT

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: "Human Cyr61 amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ser	Ser	Arg	Ile	Ala	Arg	Ala	L ^e u	Ala	L ^e u	Val	Val	Thr	L ^e u	L ^e u
1				5				10						15	

His	L ^e u	Thr	Arg	L ^e u	Ala	L ^e u	Ser	Thr	Cys	Pro	Ala	Ala	Cys	His	Cys
	20						25						30		

Pro	L ^e u	Glu	Ala	Pro	Lys	Cys	Ala	Pro	Gly	Val	Gly	L ^e u	Val	Arg	Asp
	35					40						45			

Gly	Cys	Gly	Cys	Cys	Lys	Val	Cys	Ala	Lys	Gln	L ^e u	Asn	Glu	Asp	Cys
	50					55					60				

Ser	Lys	Thr	Gln	Pro	Cys	Asp	His	Thr	Lys	Gly	L ^e u	Glu	Cys	Asn	Phe
65					70				75			80			

Gly	Ala	Ser	Ser	Thr	Ala	L ^e u	Lys	Gly	Ile	Cys	Arg	Ala	Gln	Ser	Glu
	85						90					95			

Gly	Arg	Pro	Cys	Glu	Tyr	Asn	Ser	Arg	Ile	Tyr	Gln	Asn	Gly	Glu	Ser
	100						105				110				

Phe	Gln	Pro	Asn	Cys	Gln	His	Gln	Cys	Thr	Cys	Ile	Asp	Gly	Ala	Val
	115					120					125				

Gly	Cys	Ile	Pro	L ^e u	Cys	Pro	Gln	Glu	L ^e u	Ser	L ^e u	Pro	Asn	L ^e u	Gly
	130				135					140					

Cys	Pro	Asn	Pro	Arg	L ^e u	Val	Lys	Val	Thr	Gly	Gln	Cys	Cys	Glu	Glu
145				150					155			160			

Trp	Val	Cys	Asp	Glu	Asp	Ser	Ile	Lys	Asp	Pro	Met	Glu	Asp	Gln	Asp
	165						170				175				

Gly	Leu	Leu	Gly	Lys	Glu	L ^e u	Gly	Phe	Asp	Ala	Ser	Glu	Val	Glu	Leu
	180					185					190				

Thr	Arg	Asn	Asn	Glu	L ^e u	Ile	Ala	Val	Gly	Lys	Gly	Arg	Ser	Leu	Lys
	195					200					205				

Arg	Leu	Pro	Val	Phe	Gly	Met	Glu	Pro	Arg	Ile	L ^e u	Tyr	Asn	Pro	Leu
	210				215					220					

Gln	Gly	Gln	Lys	Cys	Ile	Val	Gln	Thr	Thr	Ser	Trp	Ser	Gln	Cys	Ser
	225				230				235			240			

Lys	Thr	Cys	Gly	Thr	Gly	Ile	Ser	Thr	Arg	Val	Thr	Asn	Asn	Pro	
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245	250	255	
Glu Cys Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys			
260	265	270	
Gly Gln Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys			
275	280	285	
Thr Lys Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Leu			
290	295	300	
Ser Val Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly			
305	310	315	320
Arg Cys Cys Thr Pro Gln Leu Thr Arg Thr Val Lys Met Arg Phe Arg			
325	330	335	
Cys Glu Asp Gly Glu Thr Phe Ser Lys Asn Val Met Met Ile Gln Ser			
340	345	350	
Cys Lys Cys Asn Tyr Asn Cys Pro His Ala Asn Glu Ala Ala Phe Pro			
355	360	365	
Phe Tyr Arg Leu Phe Asn Asp Ile His Lys Phe Arg Asp			
370	375	380	

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: "Fisp12 cDNA coding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCCGCC GACAACCCCA GACGCCACCG CCTGGAGCGT CCAGACACCA ACCTCCGCC	60
CTGTCCGAAT CCAGGCTCCA GCGCGCCTC TCGTCGCCTC TGCACCCCTGC TGTGCATCCT	120
CCTACCGCGT CCCGATCATG CTCGCCTCCG TCGCAGGTCC CATCAGCCTC GCCTTGGTGC	180
TCCTCGCCCT CTGCACCCGG CCTGCTACGG GCCAGGACTG CAGCGCGCAA TGTCA GTGCG	240
CAGCCGAAGC AGCGCCGCAC TGCCCCGCCG GCGTGAGCCT GGTGCTGGAC GGCTGCGGCT	300
GCTGCCCGT CTGCGCCAAG CAGCTGGGAG AACTGTGTAC GGAGCGTGAC CCCTGCGACC	360
CACACAAGGG CCTCTTCTGC GATTTCGGCT CCCCCGCCAA CCGCAAGATT GGAGTGTGCA	420
CTGCCAAAGA TGGTGCACCC TGTGTCTTCG GTGGGTCGGT GTACCGCAGC GGTGAGTCCT	480
TCCAAAGCAG CTGCAAATAC CAATGCACTT GCCTGGATGG GGCGGTGGGC TGGGTGCCCC	540
TATGCAGCAT GGACGTGCGC CTGCCAGCC CTGACTGCC CTTCCCGAGA AGGGTCAAGC	600
TGCCTGGAA ATGCTGCAAG GAGTGGGTGT GTGACGAGCC CAAGGACCGC ACAGCAGTTG	660

GCCCTGCCCT	AGCTGCCCTAC	CGACTGGAAG	ACACATTTGG	CCCAGACCCA	ACTATGATGC	720	
GAGCCA	ACTG	CCTGGTCCAG	ACCACAGAGT	GGAGCGCCTG	TTCTAAGACC	TGTGGAATGG	780
GCATCTCCAC	CCGAGTTACC	AATGACAATA	CCTTCTGCAG	ACTGGAGAAG	CAGAGCCGCC	840	
TCTGCATGGT	CAGGCCCTGC	GAAGCTGACC	TGGAGGAAAA	CATTAAGAAG	GGAAAAAGT	900	
GCATCCGGAC	ACCTAAAATC	GCCAAGCCTG	TCAAGTTGA	GCTTTCTGGC	TGCACCAGTG	960	
TGAAGACATA	CAGGGCTAAG	TTCTGCGGGG	TGTGCACAGA	CGGCCGCTGC	TGCACACCGC	1020	
ACAGAACAC	CACTCTGCCA	GTGGAGTTCA	AATGCCCGA	TGGCGAGATC	ATGAAAAAGA	1080	
ATATGATGTT	CATCAAGACC	TGTGCCTGCC	ATTACAAC TG	TCCTGGGAC	AATGACATCT	1140	
TTGAGTCCCT	GTACTACAGG	AAGATGTACG	GAGACATGGC	GTAAAGCCAG	GAAGTAAGGG	1200	
ACACGAACTC	ATTAGACTAT	AACTTGAAC	GAGTTGCATC	TCATTTCTT	CTGTAAAAAC	1260	
AATTACAGTA	GCACATTAAT	TTAAATCTGT	GT	TTTTAACT	ACCGTGGGAG	GAACTATCCC	1320
ACCAAAGTGA	GAACGTTATG	TCATGCCAT	ACAAGTAGTC	TGTCAACCTC	AGACACTGGT	1380	
TTCGAGACAG	TTTACACTTG	ACAGTTGTT	ATTAGCGCAC	AGTGCCAGAA	CGCACACTGA	1440	
GGTGAGTCTC	CTGGAACAGT	GGAGATGCCA	GGAGAAAGAA	AGACAGGTAC	TAGCTGAGGT	1500	
TATTTTAAAA	GCAGCAGTGT	GCCTACTTT	TGGAGTGTAA	CCGGGGAGGG	AAATTATAGC	1560	
ATGCTTGCAG	ACAGACCTGC	TCTAGCGAGA	GCTGAGCATG	TGTCCCTCAC	TAGATGAGGC	1620	
TGAGTCCAGC	TGTTCTTAA	GAACAGCAGT	TTCAGCCTCT	GACCATTCTG	ATTCCAGTGA	1680	
CACTTGTCA	GAGTCAGAGC	CTTGTCTGTT	AGACTGGACA	GCTTGTGGCA	AGTAAGTTG	1740	
CCTGTAAACAA	GCCAGATTT	TATTGATATT	GTAAATATTG	TGGATATATA	TATATATATA	1800	
TATATTGT	CAGTTATCTA	AGTTAATT	AAGTCATTG	TTTTGTTTT	AAAGTCCTTT	1860	
GGGATTTAA	ACTGATAGCC	TCAAACCTCCA	AACACCATAG	GTAGGACACG	AAGCTTATCT	1920	
GTGATTCAAA	ACAAAGGAGA	TACTGCAGTG	GGAATTGTGA	CCTGAGTGAC	TCTCTGTCAG	1980	
ACAAACAAA	TGCTGTGCAG	GTGATAAAGC	TATGTATTGG	AAGTCAGATT	TCTAGTAGGA	2040	
AATGTGGTCA	AATCCCTGTT	GGTGAACAAA	TGGCCTTAT	TAAGAAATGG	CTGGCTCAGG	2100	
GTAAGGTCCG	ATTCCCTACCA	GGAAGTGCTT	GCTGCTTCTT	TGATTATGAC	TGGTTTGGGG	2160	
TGGGGGGCAG	TTTATTGTT	GAGAGTGTGA	CCAAAAGTTA	CATGTTGCA	CCTTTCTAGT	2220	
TGAAAATAAA	GTATATATAT	ATTTTTATA	TGAAAAAAA	GGAATTC		2267	

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(D) OTHER INFORMATION: "Fisp12 amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Leu Ala Ser Val Ala Gly Pro Ile Ser Leu Ala Leu Val Leu Leu
 1 5 10 15

Ala Leu Cys Thr Arg Pro Ala Thr Gly Gln Asp Cys Ser Ala Gln Cys
 20 25 30

Gln Cys Ala Ala Glu Ala Ala Pro His Cys Pro Ala Gly Val Ser Leu
 35 40 45

Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu Gly
 50 55 60

Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu Phe
 65 70 75 80

Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr Ala
 85 90 95

Lys Asp Gly Ala Pro Cys Val Phe Gly Gly Ser Val Tyr Arg Ser Gly
 100 105 110

Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp Gly
 115 120 125

Ala Val Gly Cys Val Pro Leu Cys Ser Met Asp Val Arg Leu Pro Ser
 130 135 140

Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys Cys
 145 150 155 160

Lys Glu Trp Val Cys Asp Glu Pro Lys Asp Arg Thr Ala Val Gly Pro
 165 170 175

Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro Thr
 180 185 190

Met Met Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala Cys
 195 200 205

Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp Asn
 210 215 220

Thr Phe Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg Pro
 225 230 235 240

Cys Glu Ala Asp Leu Glu Asn Ile Lys Lys Gly Lys Lys Cys Ile
 245 250 255

Arg Thr Pro Lys Ile Ala Lys Pro Val Lys Phe Glu Leu Ser Gly Cys
 260 265 270

Thr Ser Val Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr Asp
 275 280 285

Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu Phe
 290 295 300

Lys Cys Pro Asp Gly Glu Ile Met Lys Lys Asn Met Met Phe Ile Lys
 305 310 315 320

Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe Glu
 325 330 335

Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
 340 345

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2075 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: "CTGF cDNA coding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCCGGGCCGAC AGCCCCGAGA CGACAGCCCCG GCGCGTCCCG GTCCCCCACCT CCGACCACCG	60
CCAGCGCTCC AGGCCCCGCG CTCCCCGCTC GCGGCCACCG CGCCCTCCGC TCCGCCCCGCA	120
GTGCCAACCA TGACCGCCGC CAGTATGGGC CCCGTCCGCG TCGCCTTCGT GGTCCCTCCTC	180
GCCCTCTGCA GCCGGCCGGC CGTCGGCCAG AACTGCAGCG GGCGTGCCTG GTGCCCGGGAC	240
GAGCCGGCGC CGCGCTGCCG GGCAGGGCGTG AGCCTCGTGC TGGACGGCTG CGGCTGCTGC	300
CGCGTCTGCG CCAAGCAGCT GGGCGAGCTG TGCACCGAGC GCGACCCCTG CGACCCGCAC	360
AAGGGCCTCT TCTGTGACTT CGGCTCCCCG GCGAACCGCA AGATCGGCGT GTGCACCGCC	420
AAAGATGGTG CTCCCTGCAT CTTCGGTGGT ACGGTGTACC GCAGCGGAGA GTCCCTCCAG	480
AGCAGCTGCA AGTACCAAGTG CACGTGCCTG GACGGGGCGG TGGGCTGCAT GCCCCTGTGC	540
AGCATGGACG TTCTGTCTGCC CAGCCCTGAC TGCCCCCTTCC CGAGGAGGGT CAAGCTGCC	600
GGGAAATGCT GCGAGGAGTG GGTGTGTGAC GAGCCAAGG ACCAAACCGT GGTTGGGCCT	660
GCCCTCGCGG CTTACCGACT GGAAGACACG TTTGGCCAG ACCCAACTAT GATTAAGGCC	720
AACTGCCTGG TCCAGACAC AGAGTGGAGC GCCTGTTCCA AGACCTGTGG GATGGGCATC	780
TCCACCCGGG TTACCAATGA CAACGCCTCC TGCAGGCTAG AGAAGCAGAG CCGCCTGTGC	840
ATGGTCAGGC CTTGCGAAGC TGACCTGGAA GAGAACATTA AGAAGGGCAA AAAGTGCATC	900
CGTACTCCCA AAATCTCCAA GCCTATCAAG TTTGAGCTTT CTGGCTGCAC CAGCATGAAG	960
ACATACCGAG CTAAATTCTG TGGAGTATGT ACCGACGGCC GATGCTGCAC CCCCCACAGA	1020
ACCACCAACCC TGCCGGTGGG GTTCAAGTGC CCTGACGGCG AGGTCAATGAA GAAGAACATG	1080
ATGTTCATCA AGACCTGTGC CTGCCATTAC AACTGTCCCG GAGACAATGA CATCTTGAA	1140

TCGCTGTACT ACAGGAAGAT GTACGGAGAC ATGGCATGAA GCCAGAGAGT GAGAGACATT	1200
AACTCATTAG ACTGGAACCTT GAACTGATT ACATCTCATT TTTCCGTAAA AATGATTCA	1260
GTAGCACAAAG TTATTTAAAT CTGTTTTCT AACTGGGGGA AAAGATTCCC ACCCAATTCA	1320
AAACATTGTG CCATGTCAA CAAATAGTCT ATCTTCCCCA GACACTGGTT TGAAGAATGT	1380
TAAGACTTGA CAGTGGAACT ACATTAGTAC ACAGCACCAAG AATGTATATT AAGGTGTGGC	1440
TTTAGGAGCA GTGGGAGGGT ACCGGCCCGG TTAGTATCAT CAGATCGACT CTTATACGAG	1500
TAATATGCCT GCTATTTGAA GTGTAATTGA GAAGGAAAAT TTTAGCGTGC TCACTGACCT	1560
GCCTGTAGCC CCAGTGACAG CTAGGATGTG CATTCTCCAG CCATCAAGAG ACTGAGTCAA	1620
GTTGTTCCCTT AAGTCAGAAC AGCAGACTCA GCTCTGACAT TCTGATTGCA ATGACACTGT	1680
TCAGGAATCG GAATCCTGTC GATTAGACTG GACAGCTTGT GGCAAGTGAA TTTGCCTGTA	1740
ACAAGCCAGA TTTTTAAAAA TTTATATTGT AAATATTGTG TGTGTGTGTG TGTGTGTATA	1800
TATATATATA TATGTACAGT TATCTAAGTT AATTAAAGT TGTTTGTGCC TTTTTATTTT	1860
TGTTTTTAAT GCTTTGATAT TTCAATGTTA GCCTCAATT CTGAACACCA TAGGTAGAAT	1920
GTAAAGCTTG TCTGATCGTT CAAAGCATGA AATGGATACT TATATGGAAA TTCTGCTCAG	1980
ATAGAATGAC AGTCCGTCAA AACAGATTGT TTGCAAAGGG GAGGCATCAG TGTCTGGCA	2040
GGCTGATTTC TAGGTAGGAA ATGTGGTAGC TCACG	2075

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: "CTGF amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Thr	Ala	Ala	Ser	Met	Gly	Pro	Val	Arg	Val	Ala	Phe	Val	Val	Leu
1					5				10					15	

Leu	Ala	Leu	Cys	Ser	Arg	Pro	Ala	Val	Gly	Gln	Asn	Cys	Ser	Gly	Pro
					20				25				30		

Cys	Arg	Cys	Pro	Asp	Glu	Pro	Ala	Pro	Arg	Cys	Pro	Ala	Gly	Val	Ser
					35				40				45		

Leu	Val	Leu	Asp	Gly	Cys	Gly	Cys	Cys	Arg	Val	Cys	Ala	Lys	Gln	Leu
					50				55			60			

Gly	Glu	Leu	Cys	Thr	Glu	Arg	Asp	Pro	Cys	Asp	Pro	His	Lys	Gly	Leu
					65				70			75		80	

Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr
 85 90 95
 Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser
 100 105 110
 Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp
 115 120 125
 Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg Leu Pro
 130 135 140
 Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys
 145 150 155 160
 Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val Val Gly
 165 170 175
 Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro
 180 185 190
 Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala
 195 200 205
 Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp
 210 215 220
 Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg
 225 230 235 240
 Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys
 245 250 255
 Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly
 260 265 270
 Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr
 275 280 285
 Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu
 290 295 300
 Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile
 305 310 315 320
 Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe
 325 330 335
 Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
 340 345

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGGATCTGT GACGAGCCCA AGGAC

25

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGAATTCTGA CCAGGCAGTT GGCTCG

26

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGGGATCCTG TGATGAAGAC AGCATT

26

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGGAATTCAA CGATGCATTT CTGGCC

26

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asp	Gly	Cys	Gly	Cys	Cys	Lys	Val	Cys	Ala	Lys	Gln	Leu	Asn	Glu	Asp
1					5					10					15
Cys	Ser	Lys	Thr	Gln											
					20										

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Pro	Asn	Cys	Lys	His	Gln	Cys	Thr	Cys	Ile	Asp	Gly	Ala	Val	Gly	Cys
1					5				10						15
Ile	Pro	Leu	Cys	Pro											
					20										

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Cys	Ile	Val	Gln	Thr	Thr	Ser	Trp	Ser	Gln	Cys	Ser	Lys	Ser	Cys	Gly
1					5				10						15
Thr	Gly	Ile	Ser	Thr	Arg	Val	Thr								
					20										

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys Arg Leu Val Lys
1 5 10 15
Glu Thr Arg Ile Cys Glu Val Arg Pro Cys
20 25

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys Cys Thr Pro Leu Gln
1 5 10 15
Thr Arg Thr Val Lys
20

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